



1/6

ATGTCCATGA ACTGCTGAGT GGATAAACAG CACGGGATAT CTCTGTCTAA	-96
AGGAATATTA CTACACCAGG AAAAGGACAC ATTGACAAC AGGAAAGGAG	-46
CCTGTACAG AAAACCACAG TGTCTGTGC ATGTGACATT TCGCC	-1
<u>ATG GGA AAC AAC TGT TAC AAC GTG GTG GTC ATT GTG CTG CTG CTA</u>	<u>45</u>
<u>Met Gly Asn Asn Cys Tyr Asn Val Val Val Ile Val Leu Leu</u>	
<u>GTG GGC TGT GAG AAG GTG GGA GCC GTG CAG AAC TCC TGT GAT AAC</u>	<u>90</u>
<u>Val Gly Cys Glu Lys Val Gly Ala Val Gln Asn Ser Cys Asp Asn</u>	
<u>TGT CAG CCT GGT ACT TTC TGC AGA AAA TAC AAT CCA GTC TGC AAG</u>	<u>135</u>
<u>Cys Gln Pro Gly Thr Phe Cys Arg Lys Tyr Asn Pro Val Cys Lys</u>	
<u>H4-1BB FI</u>	
<u>AGC TGC CCT CCA AGT ACC TTC TCC AGC ATA GGT GGA CAG CCG AAC</u>	<u>180</u>
<u>Ser Cys Pro Pro Ser Thr Phe Ser Ser Ile Gly Gly Gln Pro Asn</u>	
<u>H4-1BB FII</u>	
<u>TGT AAC ATC TGC AGA GTG TGT GCA GGC TAT TTC AGG TTC AAG AAG</u>	<u>225</u>
<u>Cys Asn Ile Cys Arg Val Cys Ala Gly Tyr Phe Arg Phe Lys Lys</u>	
<u>TTT TGC TCC TCT ACC CAC AAC GCG GAG TGT GAG TGC ATT GAA GGA</u>	<u>270</u>
<u>Phe Cys Ser Ser Thr His Asn Ala Glu Cys Glu Cys Ile Glu Gly</u>	
<u>TTC CAT TGC TTG GGG CCA CAG TGC ACC AGA TGT GAA AAG GAC TGC</u>	<u>315</u>
<u>Phe His Cys Leu Gly Pro Gln Cys Thr Arg Cys Glu Lys Asp Cys</u>	
<u>AGG CCT GGC CAG GAG CTA ACG AAG CAG GGT TGC AAA ACC TGT AGC</u>	<u>360</u>
<u>Arg Pro Gly Gln Glu Leu Thr Lys Gln Gly Cys Lys Thr Cys Ser</u>	
<u>H4-1BB RI</u>	
<u>TTG GGA ACA TTT AAT GAC CAG AAC GGT ACT GGC GTC TGT CGA CCC</u>	<u>405</u>
<u>Leu Gly Thr Phe Asn Asp Gln Asn Gly Thr Gly Val Cys Arg Pro</u>	
<u>H4-1BB RII</u>	
<u>TGG ACG AAC TGC TCT CTA GAC GGA AGG TCT GTG CTT AAG ACC GGG</u>	<u>450</u>
<u>Trp Thr Asn Cys Ser Leu Asp Gly Arg Ser Val Leu Lys Thr Gly</u>	
<u>ACC ACG GAG AAG GAC GTG GTG TGT GGA CCC CCT GTG GTG AGC TTC</u>	<u>495</u>
<u>Thr Thr Glu Lys Asp Val Val Cys Gly Pro Pro Val Val Ser Phe</u>	
<u>TCT CCC AGT ACC ACC ATT TCT GTG ACT CCA GAG GGA GGA CCA GGA</u>	<u>540</u>
<u>Ser Pro Ser Thr Thr Ile Ser Val Thr Pro Glu Gly Gly Pro Gly</u>	
<u>GGG CAC TCC TTG CAG GTC CTT ACC TTG TTC CTG GCG CTG ACA TCG</u>	<u>585</u>
<u>Gly His Ser Leu Gln Val Leu Thr Leu Phe Leu Ala Leu Thr Ser</u>	
<u>GCT TTG CTG CTG GCC CTG ATC TTC ATT ACT CTC CTG TTC TCT GTG</u>	<u>630</u>
<u>Ala Leu Leu Leu Ala Leu Ile Phe Ile Thr Leu Leu Phe Ser Val</u>	

Fig. 1

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CTC AAA TGG ATC AGG AAA AAA TTC CCC CAC ATA TTC AAG CAA CCA <u>Leu</u> Lys Trp Ile Arg Lys Lys Phe Pro His Ile Phe Lys Gln Pro	675
TTT AAG AAG ACC ACT GGA GCA GCT CAA GAG GAA GAT GCT TGT AGC Phe Lys Lys Thr Thr Gly Ala Ala Gln Glu Glu Asp Ala Cys Ser	720
TGC CGA TGT CCA CAG GAA GAA GGA GGA GGA GGA GGC TAT GAG Cys Arg Cys Pro Gln Glu Glu Gly Gly Gly Gly Tyr Glu	765
CTG TGA Leu ---	771
 TGTACTATCC TAGGAGATGT GTGGGCCGAA ACCGAGAACG ACTAGGACCC CACCATCTG TGGAACAGCA CAACCAACCC CACCAACCTG TTCTTACACA TCATCCTAGA TGATGTGTGG GCGCGCACCT CATCCAAGTC CTTCTAACG CTAACATATT TGTCTTAC TTTTTAAAT CTTTTTTAAAT ATTAAATTT TATGTGTGTG AGTGTGTTGC CTGCCTGTAT GCACACGTGT GTGTGTGTG GTGTGTGACA CTCCTGATGC CTGAGGAGGT CAGAACGACAA AGGGTTGGTT CCATAAGAACAC TGGAGTTATG GATGGCTGTG AGCCGGNNNG ATAGGTGGG ACGGAGACACT GTCTTCCTTAT TTTAACGTGA CTGTATAATA AAAAATTT GATATTCGG GAATTGTAGA GATTGTCTG ACACCCCTCT AGTTAATGAT CTAAGGGAA TTGTTGATCA GTAGTATACT GTATATGTGT ATGTATATGT ATATGATATAT ATAAGACTCT TTTACTGTCA AAGTCACACT AGAGTGTCTG GTTACCAAGGT CAATTTATT GGACATTTA CGTCACACAC ACACACACAC ACACACACAC ACGTTTATAC TAGCTACTGT TATCGGTATT CTACGTCTATA TAATGGGATA GGGTAAAAGG AAACCAAAGA GTGAGTGTATA TTATTGGGA GGTGACAGAC TACCCCTTCT GGGTACGTAG GGACAGACCT CCTTCGGACT GTCTAAACT CCCCTTAAAGA GTCTCGTCAA GTTCCCGGAC GAAGAGGACAC GAGGAGACAC AGTCCGAAAA GTTATTTTC CGGCAAATCC TTCCCTGTT TCGTGACACT CCACCCCTTG TGACACTT TGAGTCATCC TTGGCCGGGA AGGTCAAGGTG GTACCCGTCT GTAGGGCGG GGAGACAGAG CCGCGGGGGA GCTACGAGAA TCGACTCACCA GGCGCCCGG GGCTTCGCAA ATGAAACCTTT TTTAATCTCA CAAGTTTCTG CGGGCTCGG CGGACATCTG GCGTCGATCC TTATTACCTT ATCCTGGCGC CAAGATAAAA CAACCAAAAG CCTTGACTCC GGTACTAAATT CTCCCTGCCG GCCCCGTAA GCATAACCGC GCGATCTCCA CTTTAAAGAC CTGGCCCGT TCTGCCTGGT CTGCGTTTCG TAAACGGTT TTACAAAAGT AATTAGTTCT TGCTTTCAGC CTCCAAGCTT CTGCTAGTCT ATGGCAGCAT CAAGGCTGGT ATTTCGTCAGC GCTGACCCCT ACGCCGCCGC AATAAGGGTA CTGGCCGGCC CGTCGAAGGC CCTTGGTTT CAGAAACCCA AGGCCCCCT CATAACCAACG TTTCGACTTT GATTCTTGC GGTACGTGGT GGTGGGTGCC TTAGCTTTT CTCGATAGTT AGAC	821 871 921 971 1021 1071 1121 1171 1221 1271 1321 1371 1421 1471 1521 1571 1621 1671 1721 1771 1821 1871 1921 1971 2021 2071 2121 2171 2205

*Fig. 1 Cont'd*

human homologue of mouse 4-1bb

h4-1bb Length 838

1 AATCAGCTTT GCTAGTATCA TACCTGTGCC AGATTCATC ATGGGAAACA  
51 GCTGTTACAA CATACTGCC ACTCTGTTGC TGCTCCTCAA CTTTGAGAGG  
101 ACAAGATCAT TGCAGGATCC TTGTAGTAAC TGCCCAGCTG GTACATTCTG  
151 TGATAATAAC AGGAATCAGA TTGCACTGCC CTGTCCTCCA AATAGTTCT  
201 CCAGCGCAGG TGACAAAGG ACCTGTGACA TATGCAGGCA GTGTAAGGT  
251 GTTTTCAGGA CCAGGAAGGA GTGTTCTCC ACCAGCAATG CAGAGTGTGA  
301 CTGCACTCCA GGTTTCACCA GCCTGGGGC AGGATGCAGC ATGTGTGAAC  
351 AGGATTGTAA ACAAGGTCAA GAACTGACAA AAAAAGGTTG TAAAGACTGT  
401 TGCTTTGGGA CATTAAACGA TCAGAAACGT GGCATCTGTC GACCCTGGAC  
451 AACTGTTCT TTGGATGAA AGTCTGTGCT TGTAAATGGG ACGAAGGAGA  
501 GGGACGTGGT CTGTGGACCA TCTCCAGCTG ACCTCTCTCC GGGAGCATCC  
551 TCTGTGACCC CGCTGCCCC TGCGAGAGAG CCAGGACACT CTCCGCAGAT  
601 CATCTCCCTTC TTCTTGCGC TGACGTCGAC TGCGTTGCTC TTCCCTGCTGT  
651 TCTTCCTCAC GCTCCGTTTC TCTGTGTTA AACGGGGCAG AAAGAAAACTC  
701 CTGTATATAT TCAAAACAAAC ATTATATGAGA CCACTACAAA CTACTCAAGA  
751 GGAAGATGGC TGTAGCTGCC GATTTCCAGA AGAAGAAGAA GGAGGATGTG  
801 AACTGTGAAA TGGAAAGTCAA TAGGGCTGTT GGGACTTT

Fig.2A

1 MGNSCYNIVA TLLLVLNFER TRSLQDPCSN CPAGTFCDNN RNQICSPCPP  
51 NSFSSAGGQR TCDICRQCKG VFRTRKECSS TSNAECDCTP GFHCLGAGCS  
101 MCEQDCKQGQ ELTKKGCKDC CFGTFNDQKR GICRPWTNCS LDGKSVLVNG  
151 TKERDVVCGP SPADLSPGAS SVTPPAPARE PGHSPQIISF FLALTSTALL  
201 FLLFFLTLRF SVVKGRKKL LYIFKQPFM R PVQTTQEEDG CSCRFPEEEE  
251 GGCEL

Fig.2B

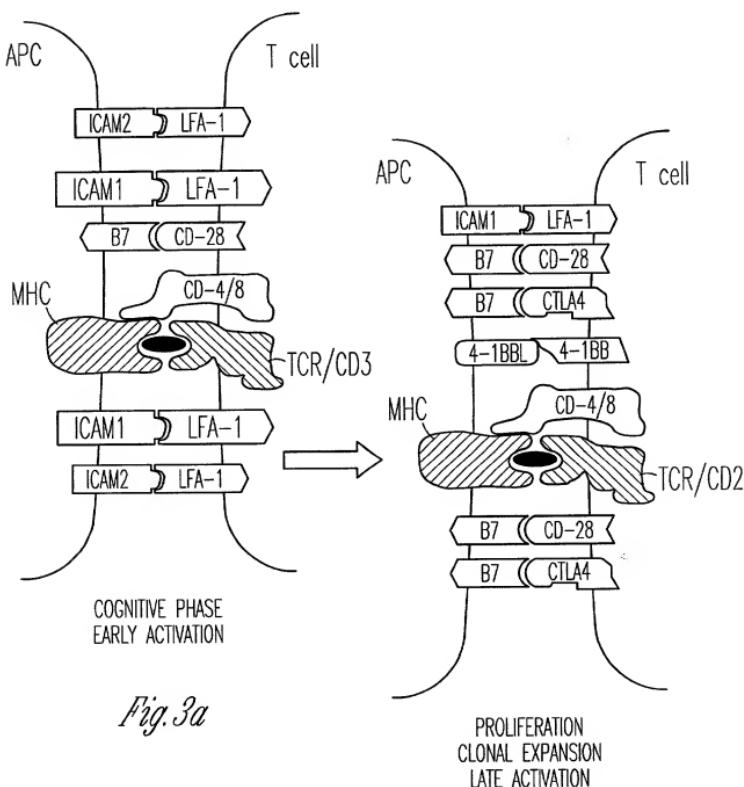


Fig. 3a

PROLIFERATION  
CLONAL EXPANSION  
LATE ACTIVATION

Fig. 3b



NORMAL T CELL ACTIVATION PATHWAY

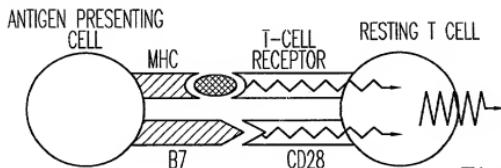


Fig. 4a

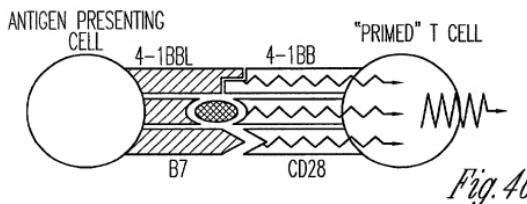


Fig. 4b

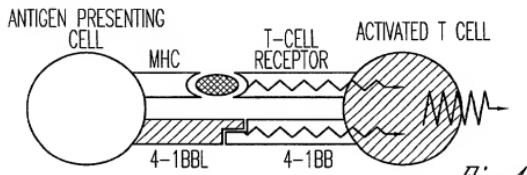


Fig. 4c

BLOCKING STEPS IN T-CELL ACTIVATION PATHWAY

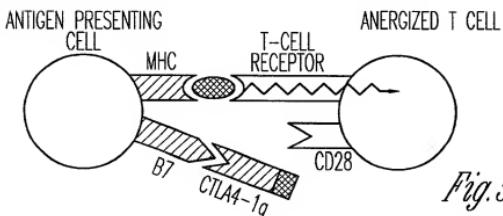


Fig. 5a

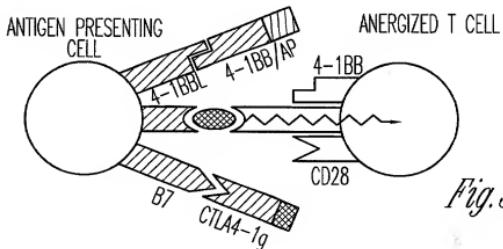


Fig. 5b

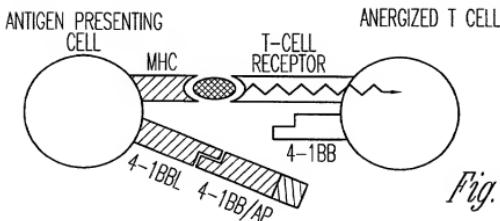


Fig. 5c